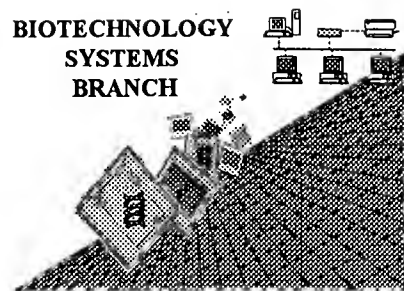


S. Turner.

RAW SEQUENCE LISTING **ERROR REPORT**

BIOTECHNOLOGY
SYSTEMS
BRANCH



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following CRF diskette:

Application Serial Number: 09/183,972

Art Unit / Team No. : 1644

Date Processed by STIC: 2/17/2000

THE ATTACHED PRINTOUT EXPLAINS THE ERRORS DETECTED.

PLEASE BE SURE TO FORWARD THIS INFORMATION TO THE APPLICANTS BY EITHER:

1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANTS ALONG WITH A NOTICE TO COMPLY or,

2) CALLING APPLICANTS AND FAXING THEM A COPY OF THE PRINTOUT WITH A NOTICE TO COMPLY

THIS WILL INSURE THAT THE NEXT SUBMISSION RECEIVED FROM THEM WILL BE ERROR FREE.

IF YOU HAVE ANY FURTHER QUESTIONS, PLEASE CALL:

MARK SPENCER 703-308-4212

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/183992

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 Wrapped Aminos The amino acid number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 Misaligned Amino Acid The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
Numbering between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 Variable Length Sequence(s) contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) feature section that some may be missing.
- 7 PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
sequence(s) . Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
to the subsequent amino acid sequence.
- 8 Skipped Sequences Sequence(s) missing. If intentional, please use the following format for each skipped sequence:
(OLD RULES) (2) INFORMATION FOR SEQ ID NO:X:
 (1) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
 (x1) SEQUENCE DESCRIPTION:SEQ ID NO:X:
 This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 Skipped Sequences Sequence(s) missing. If intentional, please use the following format for each skipped sequence.
(NEW RULES) <210> sequence Id number
 <400> sequence Id number
 000
- 10 Use of n's or Xaa's Use of n's and/or Xaa's have been detected in the Sequence Listing.
(NEW RULES) Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
 In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 Use of <213>Organism Sequence(s) are missing this mandatory field or its response.
(NEW RULES)
- 12 Use of <220>Feature Sequence(s) are missing the <220>Feature and associated headings.
(NEW RULES) Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
 Please explain source of genetic material in <220> to <223> section.
 (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

PAGE: 1

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/183,972DATE: 02/17/2000
TIME: 13:02:25

Input Set: I183972.RAW

This Raw Listing contains the General
Information Section and those Sequences
containing ERRORS.

Does Not Comply
Corrected Diskette Needed

1 <110> Hageman, Gregory S.
2 Kuehn, Markus H.
3 <120> THERAPEUTICS AND DIAGNOSTICS FOR OCULAR DISEASE BASED
4 ON A NOVEL HUMAN GENE FAMILY
5 <130> UIA-027.01
6 <140> US/09/183,972
7 <141> 1998-10-29
E--> OK 8 <160> 49
9 <170> PatentIn Ver. 2.0

ERRORED SEQUENCES FOLLOW

10 <210> 44
E--> OK 11 <211> 20
12 <212> DNA
13 <213> Artificial Sequence
14 <220>
15 <223> Description of Artificial Sequence: primer
16 delete <400> 44
17 period taaaaccca aatgcaatca 20
18 <220>
E--> OK 19 <223> Description of Artificial Sequence: primer
20 <400> 45
21 gcaggtctct ctaaacgcat g 21

E--> OK 22 <210> 46
23 <211> 15
24 <212> PRT
25 <213> Homo sapiens
26 <220>
27 <221> UNSURE
28 <222> (1)..(15)
29 <223> applicants are unsure of residues designated as
30 "Xaa" at positions 1 & 11
31 <400> 46
W--> 32 Xaa Ala Leu Phe Pro Asn Gly Val Leu Ile Xaa Pro Xaa Glu Val
33 1 5 10 15

what about Xaa at
position 13? all Xaa's
must
be explained.

See following page for more error

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/183,972

DATE: 02/18/2000
TIME: 18:33:38

Input Set: I183972.RAW

```

45      gac acc aag atg cct aca aca gaa aga gaa aca gaa ctc gct gtg tct      480
46      Asp Thr Lys Met Pro Thr Thr Glu Arg Glu Thr Glu Leu Ala Val Ser
47      145                      150                      155                      160
48      gag gag cag agg gtg gag ctc agc atc tct ctg ata aac cag agg ttc      528
49      Glu Glu Gln Arg Val Glu Leu Ser Ile Ser Leu Ile Asn Gln Arg Phe
50                      165                      170                      175
51      aag gca gag ctc gct gac tct cag tca                                555
52      Lys Ala Glu Leu Ala Asp Ser Gln Ser
53                      180                      185

```

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54 <210> SEQ ID NO 2
55 <211> LENGTH: 185
56 <212> TYPE: PRT
57 <213> ORGANISM: Callimico sp.
58 <400> SEQUENCE: 2

```

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59      Ile Phe Phe Pro Asn Gly Val Lys Val Cys Pro Gln Glu Ser Met Lys
60      1                      5                      10                      15
61      Gln Ile Leu Ala Ser Leu Gln Ala Tyr Tyr Arg Leu Arg Val Cys Gln
62                      20                      25                      30
63      Glu Ala Val Trp Glu Ala Tyr Arg Ile Phe Leu Asp Arg Ile Pro Asp
64                      35                      40                      45
65      Thr Gly Glu Tyr Gln Asp Trp Val Ser Phe Cys Gln Gln Glu Thr Phe
66                      50                      55                      60
67      Cys Leu Phe Asp Ile Gly Gln Asn Phe Ser Asn Ser Gln Glu His Leu
68                      65                      70                      75                      80
69      Asp Leu Leu Gln Gln Arg Ile Lys Gln Arg Ser Phe Pro Glu Arg Lys
70                      85                      90                      95
71      Asp Glu Val Ser Thr Glu Lys Thr Leu Gly Glu Pro Ser Glu Thr Ile
72                      100                     105                     110
73      Val Val Ser Thr Asp Val Ala Ser Val Ser Leu Gly Pro Phe Pro Val
74                      115                     120                     125
75      Thr Pro Asp Asp Thr Leu Leu Asn Glu Ile Leu Asp Asn Ala Leu Asn
76                      130                     135                     140
77      Asp Thr Lys Met Pro Thr Thr Glu Arg Glu Thr Glu Leu Ala Val Ser
78      145                      150                      155                      160
79      Glu Glu Gln Arg Val Glu Leu Ser Ile Ser Leu Ile Asn Gln Arg Phe
80                      165                      170                      175
81      Lys Ala Glu Leu Ala Asp Ser Gln Ser
82                      180                      185

```

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83 <210> SEQ ID NO 3
84 <211> LENGTH: 3261
85 <212> TYPE: DNA
86 <213> ORGANISM: Homo sapiens
87 <220> FEATURE:
88 <221> NAME/KEY: CDS
89 <222> LOCATION: (128)..(2440)
90 <400> SEQUENCE: 3

```

```

W--> 91      taaaccaaga aggttatcct caatcatctg gtatcaatat ataattattt ttccttttg 60
92      ttacttttta atgagatttg aggttggttct gtgattgtta tcagaattac catgcacaaa 120
93      agccaga atg tat ttg gaa act aga aga gct att ttt gtt ttt tgg att 169
94      Met Tyr Leu Glu Thr Arg Arg Ala Ile Phe Val Phe Trp Ile

```

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

*All items 10 on
Even summary sheet*